

Serial Number: 10/018,192

- Changed a file from non-ASCII to ASCII **ENTERED**
- Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- Edited a format error in the Current Application Data section, specifically:

- Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____.
- Added the mandatory heading and subheadings for "Current Application Data".
- Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- Changed the spelling of a mandatory field (the headings or subheadings), specifically:

- Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

- Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

- Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- Inserted colons after headings/subheadings. Headings edited included:

- Deleted extra, invalid, headings used by an applicant, specifically:

- Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file;
 page numbers throughout text; other invalid text, such as _____.
- Inserted mandatory headings, specifically: _____
- Corrected an obvious error in the response, specifically: _____
- Edited identifiers where upper case is used but lower case is required, or vice versa.
- Corrected an error in the Number of Sequences field, specifically: _____
- A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- Other:

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/018,192

DATE: 11/25/2002
TIME: 18:28:12

Input Set : N:\CrF4\11182002\J018192.raw
Output Set: N:\CRF4\11252002\J018192.raw

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1 <110> APPLICANT: Synaptic Pharmaceutical Corporation
2 <120> TITLE OF INVENTION: DNA Encoding SNORF36a and SNORF36b Receptors
3 <130> FILE REFERENCE: 59138-B-PCT/JPW
4 <140> CURRENT APPLICATION NUMBER: US/10/018,192
5 <141> CURRENT FILING DATE: 2002-11-01
6 <150> PRIOR APPLICATION NUMBER: 09/518,914
7 <151> PRIOR FILING DATE: 2000-03-03
8 <150> PRIOR APPLICATION NUMBER: 09/303,593
9 <151> PRIOR FILING DATE: 1999-05-03
10 <160> NUMBER OF SEQ ID NOS: 48
11 <170> SOFTWARE: PatentIn Ver. 2.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1508
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
17 <400> SEQUENCE: 1
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19     agctgcattgg ccaccccgac accacccaggc tggtgggaca gctcccgagag cagcatctcc 120
20     acgctggggcc ggctttccatc catcagtccc acagcacctg ggacttgggc tgctgcctgg 180
21     gtccccctcc ccacgggttga tttccagac catgccact ataccctggg cacagtgatc 240
22     ttgctgggtgg gactcacggg gatgctgggc aacctgacgg tcatctatac cttctgcagg 300
23     agcagaagcc tccggacacc tgccaaacatg ttcattatca acctcgccgt cagcgaacttc 360
24     ctcatgtcct tcacccaggc ccctgtcttc ttcaccagta gcctctataa gcagtggctc 420
25     tttggggaga caggctgcga gttctatgccc ttctgtggag ctctctttgg catttctcc 480
26     atgatcaccc tgacggccat cgccctggac cgctacctgg taatcacacgc cccgctggcc 540
27     acctttggtg tggcgtccaa gaggcgtgcgc gcattttgc tgctgggcgt ttggctctat 600
28     gccctggccct ggagtctgcc acccttcttc ggctggagcg cctacgtgccc cgaggggttg 660
29     ctgacatcct gctcctggga ctacatgagc ttcacgcccgg cctgtgcgtgc ctacaccatg 720
30     cttctctgtct gttctgttt ctccctccct ctgcttatca tcatctactg ctacatcttc 780
31     atcttcaggc ccatccggga gacaggacgg gctctccaga ctttcggggc ctgcaaggc 840
32     aatggcgagt ccctgtggca gccgcaggcg ctgcagacgg atgtcaagat ggc当地 900
33     atgctgctgg tcatcccttc ctgcgtgccc tcctgggccc cctattccgc tgtggccctg 960
34     gtggcctttt ctgggtacgc acacgtccctg acaccctaca ttagctcggt gcccaggc 1020
35     atcgccaagg cctctgcaat ccacaacccc atcatttacg ccatcaccctt ccccaagtac 1080
36     agggtggcca ttgcccagca cctgcccctgc ctgggggtgc tgctgggtgt atcaccgg 1140
37     cacagtgcgc cctaccccgat ctaccgtccc acccaccggct ccacgctgac cagccacacc 1200
38     tccaacctca gctggatctc catacggagg cgccaggagt ccctggggctc ggagagtgg 1260
39     gtgggcttggc cacacatggc ggcaggcagct gtgtggggag ctgcccagca agcaaattgg 1320
40     cggccctct acggtcaggg tctggaggac ttggaagcca aggccacccccc cagaccccg 1380
41     ggacacgaag cagagactcc agggaaagacc aaggggctga tcccccagcca ggacccagg 1440
42     atgttaggacg cccactggct ctccctttct tctgagacac atccagcccc cccacgtctc 1500
43     cctcatat                                         1508
45 <210> SEQ ID NO: 2

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RAW SEQUENCE LISTING
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DATE: 11/25/2002
TIME: 18:28:12

Input Set : N:\Crf4\11182002\J018192.raw
Output Set: N:\CRF4\11252002\J018192.raw

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46 <211> LENGTH: 478
47 <212> TYPE: PRT
48 <213> ORGANISM: Homo sapiens
49 <400> SEQUENCE: 2
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51             1           5           10          15
52     Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
53             20          25          30
54     Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
55             35          40          45
56     Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
57             50          55          60
58     Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
59             65          70          75          80
60     Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys
61             85          90          95
62     Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu
63             100         105         110
64     Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe
65             115         120         125
66     Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu
67             130         135         140
68     Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr
69             145         150         155         160
70     Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu
71             165         170         175
72     Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu
73             180         185         190
74     Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly
75             195         200         205
76     Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp
77             210         215         220
78     Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys
79             225         230         235         240
80     Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile
81             245         250         255
82     Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe
83             260         265         270
84     Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu
85             275         280         285
86     Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu
87             290         295         300
88     Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe
89             305         310         315         320
90     Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala
91             325         330         335
92     Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile
93             340         345         350
94     Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/018,192

DATE: 11/25/2002

TIME: 18:28:12

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Output Set: N:\CRF4\11252002\J018192.raw

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95          355          360          365
96 Gly Val Leu Leu Gly Val Ser Arg Arg His Ser Arg Pro Tyr Pro Ser
97          370          375          380
98 Tyr Arg Ser Thr His Arg Ser Thr Leu Thr Ser His Thr Ser Asn Leu
99          385          390          395          400
100         Ser Trp Ile Ser Ile Arg Arg Gln Glu Ser Leu Gly Ser Glu Ser
101          405          410          415
102         Glu Val Gly Trp Thr His Met Glu Ala Ala Ala Val Trp Gly Ala Ala
103          420          425          430
104         Gln Gln Ala Asn Gly Arg Ser Leu Tyr Gly Gln Gly Leu Glu Asp Leu
105          435          440          445
106         Glu Ala Lys Ala Pro Pro Arg Pro Gln Gly His Glu Ala Glu Thr Pro
107          450          455          460
108         Gly Lys Thr Lys Gly Leu Ile Pro Ser Gln Asp Pro Arg Met
109          465          470          475

111 <210> SEQ ID NO: 3
112 <211> LENGTH: 1541
113 <212> TYPE: DNA
114 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 3
116 caactcagga tgaaccctcc ttccggggcca agagtcccgc ccagccccaaac ccaagagccc 60
117 agctgcattgg ccaccccccagg accaccggc tggtgggaca gctcccaagag cagcatctcc 120
118 agcctggggcc ggcttccatc catcagtccc acagcacctg ggacttgggc tgctgcctgg 180
119 gtccccctcc ccacgggttga tggcccgacat catgcccact ataccctggg cacagtgtatc 240
120 ttgcgtgggg gactcacggg gatgctgggc aacctgacgg tcatactatac cttctgcaga 300
121 gctgtgccttc gtggagtcac tggatgtatc cagagccggaa gcctccggac acctgccaac 360
122 atgttcattta tcaaccctccg cggcagcgc tccctcatgt ctttcaccca gggccctgtc 420
123 ttcttcaccca gtagcctcta taagcagtgg ctctttgggg agacaggctg cgagttctat 480
124 gcctctgtg gagctctttt tggcatttcc tccatgtatc ccctgacggc catgccttg 540
125 gaccgctacc tggtaatcac acggcccgctg gccacctttg gtgtggcgtc caagaggcgt 600
126 gcgccatgg tccctgtggg cgtttggctc tatgccccgg cctggagtc gcccaccccttc 660
127 ttccggcttgg ggcgcctacgt gcccgggggg ttgcgtacat cctgcctctg ggactacatg 720
128 agcttcacgc cggccgtgcg tgccctacacc atgccttcct gctgtttctgt gttcttcctc 780
129 cctctgttta tcatcatcta ctgttacatc ttcatcttca gggccatccg ggagacagga 840
130 cgggtctcc agacccctgg ggcctgcaag ggcaatggcg agtccctgtg gcagcgccag 900
131 cggctgcaga gcgagtgcaa gatggccaaat atcatgtgc tggctcatctt cctttctgt 960
132 ctctccctggg ctcccttattc cgctgtggcc ctgggtggct ttgctgggtt cgcacacgtc 1020
133 ctgacaccct acatgagctc ggtgccagcc gtcatcgcca aggccctgtc aatccacaaac 1080
134 cccatcattt acggccatcac ccaccccaag tacagggtgg ccattgccccca gcacctggcc 1140
135 tgcctggggg tgctgtggg tggatcacgc cggcacagtc gccccttaccc cagctaccgc 1200
136 tccacccacc gctccacgt gaccagccac acctccaaacc tcaagctggat ctccatacgg 1260
137 aggccgccagg agtccctggg ctccggagatc gaggtgggct ggacacacat ggaggcagca 1320
138 gctgtgtggg gagctgcaca gcaagcaaat gggccgtccc tctacggta gggctctggag 1380
139 gacttggaaag ccaaggcacc ccccaagaccc cagggacacg aagcagagac tccagggaaag 1440
140 accaaggggc tgatccccag ccaggacccc agatgttagg acgcccactg gctctccctt 1500
141 tcttctgaga cacatccagc ccccccacgt ctccctcata t 1541

143 <210> SEQ ID NO: 4
144 <211> LENGTH: 489
145 <212> TYPE: PRT

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/018,192

DATE: 11/25/2002
TIME: 18:28:12

Input Set : N:\CrF4\11182002\J018192.raw
Output Set: N:\CRF4\11252002\J018192.raw

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146 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 4
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149      1           5           10          15
150 Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
151      20          25          30
152 Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
153      35          40          45
154 Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
155      50          55          60
156 Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
157      65          70          75          80
158 Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys
159      85          90          95
160 Arg Ala Val Leu Arg Gly Val Thr Val Met Met Gln Ser Arg Ser Leu
161      100         105         110
162 Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu Ala Val Ser Asp Phe
163      115         120         125
164 Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe Thr Ser Ser Leu Tyr
165      130         135         140
166 Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu Phe Tyr Ala Phe Cys
167      145         150         155         160
168 Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr Leu Thr Ala Ile Ala
169      165         170         175
170 Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu Ala Thr Phe Gly Val
171      180         185         190
172 Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu Gly Val Trp Leu Tyr
173      195         200         205
174 Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly Trp Ser Ala Tyr Val
175      210         215         220
176 Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp Tyr Met Ser Phe Thr
177      225         230         235         240
178 Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys Cys Phe Val Phe Phe
179      245         250         255
180 Leu Pro Leu Leu Ile Ile Tyr Cys Tyr Ile Phe Ile Phe Arg Ala
181      260         265         270
182 Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe Gly Ala Cys Lys Gly
183      275         280         285
184 Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu Gln Ser Glu Cys Lys
185      290         295         300
186 Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu Phe Val Leu Ser Trp
187      305         310         315         320
188 Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe Ala Gly Tyr Ala His
189      325         330         335
190 Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala Val Ile Ala Lys Ala
191      340         345         350
192 Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile Thr His Pro Lys Tyr
193      355         360         365
194 Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu Gly Val Leu Leu Gly

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RAW SEQUENCE LISTING

DATE: 11/25/2002

PATENT APPLICATION: US/10/018,192 TIME: 18:28:12

Input Set : N:\Crf4\11182002\J018192.raw
 Output Set: N:\CRF4\11252002\J018192.raw

195	370	375	380
196	Val Ser Arg Arg His Ser Arg Pro Tyr Pro Ser Tyr Arg Ser Thr His		
197	385	390	395
198	Arg Ser Thr Leu Thr Ser His Thr Ser Asn Leu Ser Trp Ile Ser Ile		400
199	405	410	415
200	Arg Arg Arg Gln Glu Ser Leu Gly Ser Glu Ser Glu Val Gly Trp Thr		
201	420	425	430
202	His Met Glu Ala Ala Ala Val Trp Gly Ala Ala Gln Gln Ala Asn Gly		
203	435	440	445
204	Arg Ser Leu Tyr Gly Gln Gly Leu Glu Asp Leu Glu Ala Lys Ala Pro		
205	450	455	460
206	Pro Arg Pro Gln Gly His Glu Ala Glu Thr Pro Gly Lys Thr Lys Gly		
207	465	470	475
208	Leu Ile Pro Ser Gln Asp Pro Arg Met		480
209	485		
211 <210>	SEQ ID NO: 5		
212 <211>	LENGTH: 250		
213 <212>	TYPE: DNA		
214 <213>	ORGANISM: Rattus norvegicus		
215 <400>	SEQUENCE: 5		
216	catagccatg gaccgctatac tgggtgatcac acgtccactg gccaccatcg gcatgagatc	60	
217	caagagacgg acggcactag tcctgctagg tgtctggctc tatgccctgg cctggagtct	120	
218	gcccgccttc tttggctgga ggcctacgt gcccgggggg ctgctgacat cctgctcctg	180	
219	ggactacgtg accttcacgc ccctcgtgcg cgcctacacc atgctgctct tctgctttgt	240	
220	cttcttcctc		250
222 <210>	SEQ ID NO: 6		
223 <211>	LENGTH: 83		
224 <212>	TYPE: PRT		
225 <213>	ORGANISM: Rattus norvegicus		
226 <400>	SEQUENCE: 6		
227	Ile Ala Met Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu Ala Thr Ile		
228	1 5 10 15		
229	Gly Met Arg Ser Lys Arg Arg Thr Ala Leu Val Leu Leu Gly Val Trp		
230	20 25 30		
231	Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly Trp Ser Ala		
232	35 40 45		
233	Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp Tyr Val Thr		
234	50 55 60		
235	Phe Thr Pro Leu Val Arg Ala Tyr Thr Met Leu Leu Phe Cys Phe Val		
236	65 70 75 80		
237	Phe Phe Leu		
239 <210>	SEQ ID NO: 7		
240 <211>	LENGTH: 1473		
241 <212>	TYPE: DNA		
242 <213>	ORGANISM: Rattus norvegicus		
243 <400>	SEQUENCE: 7		
244	ttaagtcc tcaagacgc gagcatgaac tctccctcag aatcaagagt cccttcaagc	60	
245	ttaactcagg atcccagctt taccgccagc cctgcctcc tacaaggcat ttgaaacagc	120	
246	actcagaaca tctccgtcag agtccagctt ctatccgtta gccccacgac acctggcgtt	180	

VERIFICATION SUMMARY

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